

Sequence Comparison for US. 6,794,501

us-10-007-047-1.rni

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 02:15:21 ; Search time 689 Seconds
(without alignments)
10767.603 Million cell updates/sec

Title: US-10-007-047-1

Perfect score: 4534

Sequence: 1 ccaagcttggtaaaaaaaa.....gcatgcnnatagaggcccta 4534

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
1	3855	85.0	6628	4	US-09-949-016-4586	Sequence 4586, Ap
2	3754.8	82.8	4796	3	US-09-085-199B-3	Sequence 3, Appli
3	1664.4	36.7	2301	3	US-09-085-199B-8	Sequence 8, Appli
4	1155.2	25.5	1164	3	US-09-085-199B-1	Sequence 1, Appli
5	1118.4	24.7	3715	3	US-09-085-199B-44	Sequence 44, Appli
6	1116.8	24.6	68702	4	US-09-949-016-16328	Sequence 16328, A
7	970	21.4	3979	3	US-09-085-199B-10	Sequence 10, Appli
8	715.4	15.8	3876	4	US-09-849-602-4	Sequence 4, Appli
9	483.2	10.7	3251	3	US-09-085-199B-6	Sequence 6, Appli
10	187	4.1	436	3	US-09-085-199B-28	Sequence 28, Appli
c 11	187	4.1	601	4	US-09-949-016-163605	Sequence 163605,
12	175.4	3.9	279	3	US-09-085-199B-43	Sequence 43, Appli
13	149	3.3	485	3	US-09-085-199B-32	Sequence 32, Appli
14	147.2	3.2	193	3	US-09-085-199B-17	Sequence 17, Appli
15	144.6	3.2	578	3	US-09-085-199B-25	Sequence 25, Appli
16	144	3.2	565	3	US-09-085-199B-23	Sequence 23, Appli
17	138.8	3.1	498	3	US-09-085-199B-36	Sequence 36, Appli

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18	136.6	3.0	468	3	US-09-085-199B-33	Sequence 33, Appl
19	126.6	2.8	418	3	US-09-085-199B-42	Sequence 42, Appl
c 20	126.2	2.8	601	4	US-09-949-016-163634	Sequence 163634,
c 21	125	2.8	359	3	US-09-085-199B-30	Sequence 30, Appl
c 22	116	2.6	510	4	US-09-270-767-928	Sequence 928, App
c 23	116	2.6	510	4	US-09-270-767-16210	Sequence 16210, A
c 24	114	2.5	427	3	US-09-085-199B-37	Sequence 37, Appl
c 25	113.4	2.5	601	4	US-09-949-016-163645	Sequence 163645,
c 26	113.4	2.5	601	4	US-09-949-016-163646	Sequence 163646,
c 27	113.4	2.5	601	4	US-09-949-016-163647	Sequence 163647,
c 28	111.2	2.5	421	3	US-09-085-199B-35	Sequence 35, Appl
c 29	111.2	2.5	601	4	US-09-949-016-163613	Sequence 163613,
30	110.8	2.4	351	3	US-09-085-199B-41	Sequence 41, Appl
31	105.6	2.3	437	3	US-09-085-199B-40	Sequence 40, Appl
32	104.2	2.3	209	3	US-09-085-199B-31	Sequence 31, Appl
c 33	103	2.3	601	4	US-09-949-016-163567	Sequence 163567,
c 34	102	2.2	390	3	US-09-085-199B-26	Sequence 26, Appl
c 35	102	2.2	601	4	US-09-949-016-163602	Sequence 163602,
c 36	98.6	2.2	502	3	US-09-085-199B-39	Sequence 39, Appl
c 37	98.6	2.2	601	4	US-09-949-016-163624	Sequence 163624,
c 38	98.6	2.2	601	4	US-09-949-016-163626	Sequence 163626,
c 39	98.6	2.2	601	4	US-09-949-016-163627	Sequence 163627,
c 40	98.2	2.2	601	4	US-09-949-016-163625	Sequence 163625,
c 41	92.8	2.0	393	3	US-09-085-199B-34	Sequence 34, Appl
c 42	90.8	2.0	8078	3	US-09-702-251-3	Sequence 3, Appl
c 43	89.4	2.0	469	3	US-09-085-199B-29	Sequence 29, Appl
c 44	80.4	1.8	327	3	US-09-085-199B-20	Sequence 20, Appl
c 45	79.8	1.8	3489	2	US-08-728-323A-1	Sequence 1, Appl

RESULT 8

US-09-849-602-4

; Sequence 4, Application US/09849602

; Patent No. 6794501

; GENERAL INFORMATION:

; APPLICANT: Scanlan, Matthew J.

; APPLICANT: Old, Lloyd J.

; APPLICANT: Stockert, Elisabeth

; APPLICANT: Chen, Yao-Tseng

; TITLE OF INVENTION: Colon Cancer Antigen Panel

; FILE REFERENCE: L0461/7105(JRV)

; CURRENT APPLICATION NUMBER: US/09/849,602

; CURRENT FILING DATE: 2001-05-04

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 3876

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-849-602-4

Query Match 15.8%; Score 715.4; DB 4; Length 3876;
 Best Local Similarity 56.9%; Pred. No. 1e-190;
 Matches 1458; Conservative 0; Mismatches 1006; Indels 99; Gaps 4;

Qy	619 ATGTTTGACTACCTGGAGTGTGAACCTAACCTCTTCCAAACAGTATTCAACTCCCTGGAC 678
Db	1 ATGTTTGATTACATGGATTGTGAGCTGAAGCTTCTGAATCAGTTTCCGACAGCTAAC 60
Qy	679 ATGTCCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCTGCCCGCTGATCCAG 738
Db	61 ACGGCCATGCCGTATCCCAGATGTCCTCAGGCCAGTGCCGCCTGCCGCCCTCATCCAG 120

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Qy	739	GTCATCTTGGACTGCAGCCACCTTATGACTACACTGTCAAGCTCTTCAAACCTCAC	798
Db	121	GTCATCCAGGACTGCAGCCACCTCTACCACTACACGGTCAAGCTCTGTTCAAGCTACAC	180
Qy	799	TCCCTGCCCTCCCAGCTGACACCCTGAAGGCCACCGGGACCGCTTATGGAGCAGTTACA	858
Db	181	TCTTGTCTCCCTGGGACACCCCTGAAGGCCACAGGGACCGGTTCCACGAGCAGTTCAC	240
Qy	859	AAGTTGAAAGATCTGTTCTACCGCTCAGCAACCTGCAGTACTTCAAGCGGCTATTCA	918
Db	241	AGCCTCAGGAACCTCTTCCGAGAGCCTCGACATGCTGTACTTCAAGCGGCTCATCCAG	300
Qy	919	ATCCCCCAGCTGCCCTGAGAACCCACCCAACTTCCCTGCGAGCCTCAGCCCTGTCAGAACAT	978
Db	301	ATCCCCCGGCTGCCGAGGGACCCCTAACCTTCCCTGCGGGCCTCAGCCCTGGCTGAGCAC	360
Qy	979	ATCAGCCCTGTGGTGGTATCCCTGCAGAGGCCCTCATCCCCGACAGCGAGCCAGTCCTA	1038
Db	361	ATCAAGCCGGTGGTGGTATCCCCGAGGGAGGGCCCC-----GGAAGATGAG	405
Qy	1039	GAGAAGGGATGACCTCATGGACATGGATGCCCTCAGCAGAATTATTGACAACAAGTT	1098
Db	406	GAGCCGGAGAACATCTCATTGAGATCAGCACAGGGCCCCCGCGGGGGAGCCAGTGGTGGT	465
Qy	1099	GATGACATCTTGGCAGTTATTGAGCAGTGTCCATTCAACAGTCAAATGGT	1158
Db	466	GCTGACCTCTCGATCAGACGTTGG-----ACCCCCCAATGGG	504
Qy	1159	GTGAACAAGGATGAGAACGGACACTTAATTGAGCGACTATAAGAGAGATCAGTGGATTG	1218
Db	505	TCTGTGAAGGACGACAGGGACCTCCAGATTGAGAGCTTGAAAGAGAGAGGTGGAAATGCTC	564
Qy	1219	AAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGTGCTGCAGCTGAAGGGC	1278
Db	565	CGCTCTGAACCTGGAGAACATCAAGCTGGAGGCCAGCGGTACATCGCGCAGCTGAAGAGC	624
Qy	1279	CACGTCAGCGAGCTGGAGCAGATCTGGCCAGCAGCAGCACCTGCGGCAGCAGGCC	1338
Db	625	CAGGTGAATGCACTGGAGGGTAGCTGGAGGAGCAGCGGAAGCAGAAGCAGAAGGCCCTG	684
Qy	1339	GACGACTGTGAATTCCCTGCGGGCAGAACTGGACGAGCTCAGGAGGCAGCGGGAGGACACC	1398
Db	685	GTGGATAATGAGCAGCTCCGCCACGAGCTGGCCAGCTGAGGGCTGCCAGCTGGAGGGC	744
Qy	1399	GAGAAGGCTCAGCGGAGCCTGCTGAGATAGAAAGGAAAGCTCAAGCCAATGAACAGCGA	1458
Db	745	GAGCGGAGCCAGGGCTGGTAGAGGAGGCTGAGAGGAAGGCCAGTGCCACGGAGGCCGC	804
Qy	1459	TATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACACCGCTGACCTGCTGCGG	1518
Db	805	TACAACAAGCTGAAGGAAAGACAGTGAGCTCGTCCATGTGACCGGAGCTGCTCAGA	864
Qy	1519	AAGAATGCAGAGGTGACCAAACAGGTGTCATGCCAGACAAGCCCAGGTAGATTGGAA	1578
Db	865	AAGAACCGGGACACAGCCAAGCAGCTGACGGTGACGCAGCAAAGCCAGGAGGAGGTGGCG	924
Qy	1579	CGAGAGAAAAAGAGCTGGAGGATTGTTGGAGCGCATCAGTGACCAAGGGCCAGCGGAAG	1638
Db	925	CGGGTGAAGGAGCAGCTGCCCTCCAGGTGGAGCAGGTGAAGCGGGAGTCGGAGTTGAAG	984
Qy	1639	ACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACCTGCCACAAGCCAACGG	1698

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Db	985	CTAGAGGAGAAGAGCGACCAGCTGGAGAACGCTCAAGAGGGAGCTGGAGGCCAAGGCCGA	1044
Qy	1699	GAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCAGTCAGAACAACTGGCA	1758
Db	1045	GAGCTGGCCCGCGCAGGAGGCCCTGAGCCACACAGAGCAGAGCAAGTCGGAGCTGAGC	1104
Qy	1759	GCCGAGTTGCCGAGCTAGAGAACGGAGCGGGACAGCCTGGTGAGTGGCGCAGCTCATAGG	1818
Db	1105	TCACGGCTGGACACGCTGAGTCGGAGAACGGATGCTCTGAGTGGAGCTGTGCGGCAGCGG	1164
Qy	1819	GAGGAGGAATTATCTGCTCTCGAACAGAACACTGCAGGACACTCAGCTCAAACGGCCAGC	1878
Db	1165	GAGGCAGACCTGCTGGCGGCAGAGCCTGGTGCGAGACAGAGGCCGCTGAGCCGG	1224
Qy	1879	ACAGAG-----GAATCTATGTGCCAGCTTGCCAAAGACCAA	1914
Db	1225	GAGCAGCAGCGCAGCTCCCAGGAGCAGGGCGAGTTGCAGGGCCGGCTGGCAGAGAGGGAG	1284
Qy	1915	CGAAAAATGCTCTGGTGGGTCCAGGAAGGCTGGAGCAG-----	1956
Db	1285	TCTCAGGAGCAGGGCTGCGCAGAGGCTGCTGGACGAGCAGTCGAGTGTGCGGGC	1344
Qy	1957	-----GTGATACAAGACGCCCTGAACCAGCTTGAAGAACCTCCT	1995
Db	1345	GCTGCTGCCAGGCCGCGGCATCCTGCAGGATGCCGTGAGCAAGCTGGACGACCCCCCTG	1404
Qy	1996	CTCATCAGCTGCCCTGGGCTGCAGATCACCTCCCTCCACGGTCACATCCATTCCAGC	2055
Db	1405	CACCTGCGCTGTACCAAGCTCCCAGACTACCTGGTGAGCAGGGCCAGGAGGCCCTGGAT	1464
Qy	2056	TGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCAGAACACATCAGT	2115
Db	1465	GCCGTGAGCACCCCTGGAGGAGGGCACGCCAGTACCTGACCTCCTGGCAGACGCCCTCC	1524
Qy	2116	GGACTTCTCCATTCCATAACCCCTGCTGGCCCACTTGACCAGCGACGCCATTGCTCATGGT	2175
Db	1525	GCCCTGGTGGCAGCTCTGACCCGTTCTCCACCTGGCTGCCAGACATCATCAATGGC	1584
Qy	2176	GCCACCCACCTGCCCTAGAGCCCCACCTGAGCCTGCCACTCACTGACCGAGGCCCTGTAAG	2235
Db	1585	GGTGCACCTCGCACCTGGCTCCACCGACCCCTGCCACGCCCTCATAGACACCTGCAGG	1644
Qy	2236	CAGTATGGCAGGGAAACCCCTGCCAACCTGGCCTCCCTGGAGGAAGAGGGAGCCTTGAG	2295
Db	1645	GAGTGGGGGCCGGCTCTGGAGCTCATGGGGCAGCTGCAGGACCAGCAGGCTCTGGCG	1704
Qy	2296	AATGCCGACAGCACGCCATGAGGAACCTGCCAGCAAGATCAAGGCCATGGCGAGGAG	2355
Db	1705	CACATGCAGGCCAGCCTGGTGGACACCCCTGCAGGGCATCCTCAGCTGGCCAGGAA	1764
Qy	2356	CTCCTGCCAGGGACTGGACATCAAGCAGGAGGAGCTGGGGACCTGGTGACAAGGAG	2415
Db	1765	CTGAAACCCAAGAGCCTAGATGTGCGCAGGAGGAGCTGGGGCCGTGGTCACAAGGAG	1824
Qy	2416	ATGGCGGCCACTTCAGCTATTGAAACTGCCACGCCAGAACATAGAGGAGATGCTCAGC	2475
Db	1825	ATGGCGGCCACATCCGCAGCCATTGAAGATGCTGTGCGGAGGATTGAGGACATGATGAAC	1884
Qy	2476	AAATCCGAGCAGGAGAACAGGAGTCAAATTGGAGGTGAATGAAAGGATCCTGGTTGC	2535
Db	1885	CAGGCACGCCACGCCAGCTGGGGGTGAAGCTGGAGGTGAACGAGAGGATCCTCAACTCC	1944
Qy	2536	TGTACCAGCCTCATGCAAGCTATTCAAGTGCTCATCGTGGCCTCTAAGGACCTCCAGAGA	2595

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Db	1945	TGCACAGACCTGATGAAGGCTATCGGCTCTGGTACGACATCCACTAGCCTGCAGAAG 2004
Qy	2596	GAGATTGTGGAGAGCGGCAGGGTACAGCATCCCCTAAAGAGTTTATGCCAAGAACTCT 2655
Db	2005	GAGATCGTGGAGAGCGGCAGGGGGCAGCCACGCAGCAGGAATTACGCCAAGAACTCG 2064
Qy	2656	CGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGAGGCCACTGTCATG 2715
Db	2065	CGCTGGACCGAAGGCCTCATCTGGCCTCCAAGGCTGTGGGCTGGGAGGCCACACAGCTG 2124
Qy	2716	GTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTGAGGAGCTAATGGTGTGT 2775
Db	2125	GTGGAGGCAGCTGACAAGGTGGTCTTACACGGCAAGTATGAGGAGCTATCGTCTGC 2184
Qy	2776	TCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGCTGGCTGCATCCAAGGTGAAAGCTGAT 2835
Db	2185	TCCCACGAGATCGCAGCCAGCACGGCCAGCTGGGGGGCTCCAAGGTGAAGGCCAAC 2244
Qy	2836	AAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCCTCTGGGAGTGAACCAGGCCACT 2895
Db	2245	AAGCACAGCCCCACCTGAGCCGCTGCAGGAATGTTCTGCACAGTCATGAGAGGGCT 2304
Qy	2896	GCCGGCGTTGTGGCCTCAACCATTCCGGCAAATCACAGATCGAAGAGACAGACAACATG 2955
Db	2305	GCCAATGTGGTGGCCTCCACCAAGTCAGGCCAGGAGCAGATTGAGGACAGAGACACCATG 2364
Qy	2956	GACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGATTCTCAGGTTAGG 3015
Db	2365	GATTTCTCGGCCTGTCCCTCATCAAGCTGAAGAAGCAGGAGATGGAGACGCAGGTGCGT 2424
Qy	3016	GTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTAAAAACTGGGAGAGCTTCGGAAA 3075
Db	2425	GTCCTGGAGCTGGAGAAGACGCTGGAGGCTAACGCATGCCCTGGGGAGTTGCGGAAG 2484
Qy	3076	AAGCACTACGAGCTTGTGGTGTGCTGAGGGCTGGGAAGAAG 3118
Db	2485	CAACACTACGTGGCTGGCATCAGGCAGCCCTGGAGAGG 2527